In those embodiments of the invention directed to production of a protein for quantitative assay or purification, it is most desired that cells that do not secrete proteases are used. Preferred host cells are COS, CHO, NIH/3T3, *Drosophila* cells, especially Schneider 2 cells, piscine epithelial cells (EPC) and yeast cells, such as *S. cerevisiae* and *S. pombe* and *Pichia* spp., especially protease-deficient yeast cells.

IN THE CLAIMS:

Cancel claims 1-9, 11-13, 15-17, and 26-29, without prejudice.

Add new claims 30-54.

30. An isolated nucleic acid comprising a nucleotide sequence encoding a secretory signal sequence comprising the amino acid sequence SEQ ID NO:10, or variants of said amino acid sequence that comprise conservative replacements thereof that retain the biological activities of directing secretion of a fusion protein from a cell and cleavage of the secretory signal sequence from the fusion protein, wherein the variations in said variants

(a) relate to the G and D residues constituting the cleavage site, and in said variations G and/or D are retained or D is replaced by E and/or G is replaced by A or V,

(b) constitute at most 4 additions or deletions of amino acids in the secretory sequence,

(c) result in the stretch of hydrophobic amino acids in the interior of the secretory sequence being 10-15 amino acids long, and/or

(d) constitute the overall substitution of fewer than 7 amino acids in the secretory sequence.

31. The isolated nucleic acid of claim 30, wherein the arginine at the second position is replaced by lysine and/or the glycine at the fifteenth position is replaced by alanine or valine and/or the aspartic acid at the sixteenth position is replaced by glutamic acid.

32. The isolated nucleic acid of claim 31, wherein the amino acid sequence is the amino acid sequence of SEQ ID NO:10.

33. The isolated nucleic acid of claim 30, wherein the nucleotide sequence encoding the secretory signal sequence is SEQ ID NO:11.

34. The isolated nucleic acid of claim 30, wherein the cell from which secretion is directed is a eukaryotic cell.

35. The isolated nucleic acid of claim 30, wherein the cell from which secretion is directed is a prokaryotic cell.

36. The isolated nucleic acid of claim 32, wherein the secretory signal sequence is cleaved between the G and D residues in the VGDQ portion thereof.

37. An isolated nucleic acid comprising a nucleotide sequence encoding a fusion protein comprising a secretory signal sequence and a desired heterologous protein,
wherein said secretory signal sequence comprises the amino acid sequence SEQ ID NO:10, or variants of said amino acid sequence that comprise conservative replacements thereof that retain the biological activities of directing secretion of a fusion protein from a cell and cleavage of the secretory signal sequence from the fusion protein, wherein the variations in said variants

(a) relate to the G and D residues constituting the cleavage site, and in said variations G and/or D are retained or D is replaced by E and/or G is replaced by A or V,

(b) constitute at most 4 additions or deletions of amino acids in the secretory sequence,

(c) result in the stretch of hydrophobic amino acids in the interior of the secretory sequence being 10-15 amino acids long, and/or

(d) constitute the overall substitution of fewer than 7 amino acids in the secretory sequence, and

wherein the desired heterologous protein is joined to the carboxy-terminus of the secretory signal sequence, either directly or by a linking amino acid sequence.

38. The isolated nucleic acid of claim 37, wherein said secretory signal sequence comprises the amino acid sequence SEQ ID NO:10, or variants of said amino acid sequence wherein the arginine at the second position is replaced by lysine and/or the glycine at the fifteenth position is replaced by alanine or valine and/or the aspartic acid at the sixteenth position is replaced by glutamic acid.

39. The isolated nucleic acid of claim 38, wherein said amino acid sequence is the amino acid sequence of SEQ ID NO:10.

40. The isolated nucleic acid of claim 39, wherein the nucleotide sequence encoding the secretory signal sequence is SEQ ID NO:11.

41. The isolated nucleic acid of claim 37 wherein said desired heterologous protein is a reporter protein.

42. The isolated nucleic acid of claim 41, wherein the reporter protein is selected from the group consisting of chloramphenicol aminotransferase, green fluorescent protein or another aequorin, β-amylase, β-lactamase, luciferase, glucuronidase, alkaline phosphatase, and ß-galactosidase.

43. The isolated nucleic acid of claim 37 wherein said desired protein is a lipopolysaccharide-binding protein.

44. The isolated nucleic acid of claim 43, wherein the lipopolysaccharide-binding protein is Factor C.

45. A recombinant vector comprising the isolated nucleic acid of any one of claims 37-40.

46. A host cell transformed with the recombinant vector of claim 45.

47. The recombinant host cell of claim 46, wherein said cell is selected from the group consisting of a bacterial cell, a COS cell, a Chinese hamster ovary (CHO) cell, a NIH/3T3 cell, a Schneider 2 cell, a *S. cerevisiae* cell, and an endothelial progenitor cell (EPC).

48. A method for producing a desired protein comprising

culturing a host cell of claim 46 under conditions wherein the desired protein is secreted from the host cell, and

recovering the desired protein from the culture medium.

49. A fusion protein comprising

(i) a secretory signal sequence polypeptide comprising the amino acid sequence SEQ ID NO:10, or variants of said amino acid sequence that

comprise conservative replacements thereof that retain the biological activities of directing secretion of a fusion protein from a cell and cleavage of the secretory signal sequence from the fusion protein, wherein the variations in said variants

(a) relate to the G and D residues constituting the cleavage site, and in said variations G and/or D are retained or D is replaced by E and/or G is replaced by A or V,

(b) constitute at most 4 additions or deletions of amino acids in the secretory sequence,

(c) result in the stretch of hydrophobic amino acids in the interior of the secretory sequence being 10-15 amino acids long, and/or

(d) constitute the overall substitution of fewer than 7 amino acids in the secretory sequence, and

(ii) a heterologous polypeptide.

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50. The fusion protein of claim 49, wherein said secretory signal sequence polypeptide comprises the amino acid sequence SEQ ID NO:10, or variants of said amino acid sequence wherein the arginine at the second position is replaced by lysine and/or the glycine at the fifteenth position is replaced by alanine or valine and/or the aspartic acid at the sixteenth position is replaced by glutamic acid.

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51. The fusion protein of claim 50, wherein said amino acid sequence is the amino acid sequence of SEQ ID NO:10.

52. The fusion protein of claim 51, wherein the nucleotide sequence encoding the secretory signal sequence is SEQ ID NO:11.

53. The fusion protein of claim 49, wherein the heterologous polypeptide is a lipopolysaccharide binding protein.

54. The fusion protein of claim 49, wherein the heterologous polypeptide is a protein selected from the group consisting of chloramphenicol aminotransferase, green fluorescent protein or another aequorin, β-amylase, β-lactamase, luciferase, glucuronidase, alkaline phosphatase, and ß-galactosidase.